

PC-500



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,945

DATE: 08/14/2002
TIME: 11:43:30

Input Set : A:\10624092999.txt
Output Set : N:\CRF4\08142002\J009945.raw

3 <110> APPLICANT: Thomsen, Gerald
4 Wrana, Jeffery
6 <120> TITLE OF INVENTION: ANTAGONISTS OF BMP AND TGF-BETA SIGNALING PATHWAYS
8 <130> FILE REFERENCE: 10624-092
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/009,945
C--> 10 <141> CURRENT FILING DATE: 2002-06-21
10 <160> NUMBER OF SEQ ID NOS: 13
12 <170> SOFTWARE: PatentIn version 3.1
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 2172
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
19 <220> FEATURE:
20 <223> OTHER INFORMATION: Human Smurf1
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25 cactcaacccg acaactgtgaa aaacacattg gaccocaaagt ggaaccagca ctatgatcta 180
26 tatgtttgga aaacggatct gataaccatt agcgtgtgga accataagaa aattcacaag 240
27 aaacaggggag ctggcttcctt gggtgtgtgt cgggtgctct ccaatgccat cagcagatta 300
28 aaagataccg gataccagcg tttggatcta tgc aaactaa acccctcaga tactgatgca 360
29 gtctgtggcc agatagtgtt cagttttacag acacagagaca gaataggaa cggcgctctg 420
30 gtggtggaat gcagaggact gttgaaaaat gaaggaaacgg tgtatgaaga ctccgggcct 480
31 ggaggggccgc tcagctgctt catggaggaa ccagcccctt acacagatag caccgggtgt 540
32 gctgtgggag gagggaattg caggttctgt gagtccccaa gtcaagatca aagacttcaag 600
33 gcacagcgccg tgcgaaaccc tgatgtgcga ggttcactac agacgcccac gaaccgacca 660
34 caccggccacc agtcccgcga actgcgccga ggctacgaac aaagaacaa acgtccagggc 720
35 caagtttact ttttgatac acagactgga gttagacgtt ggcaacgccc caggatacca 780
36 agagaccotta acagtgtgaa ctgtgatgaa cttggaccac tgcgcgcagg ctgggaagtc 840
37 agaagtacag tttctgggag gatataattt gtatgacata ataaccgaac aaccagttt 900
38 acagaccocaa ggttacacca catcatgaat caccagtgcc aactcaaggga gccaccgacg 960
39 ccgtgtgccac tgcacagtgga gggtctctct gaggacgagg agcttctcgc ccagagatca 1020
40 gaaagagatc tatgccagaa gctgaaagtc ctcaagacacg aactgtcgtc tcagacgccc 1080
41 caagctgggtc attgcgcgat cgaagtgtcc agagaagaaa tctttgagga gtcttaccgc 1140
42 cagataatga agatgcgacc gaaagaattg aaaaaacggc tgatgtgtgaa attccgtggg 1200
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48 ctgataaaga gcttgggtgt gatccatagag aacgacatca cgcctgtact ggaccaacac 1560
49 tctgcgtgtg aacacacgcg cttcggggcg attcctgacg atgaactgtg acccaatggc 1620
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51 aggtttatga gaggaatcga agcccagttc ttactctgc agaaggggtt caatgagctc 1740
52 atccctcaac atctgctgaa gccttttgac cagaaggaac tggagctgat cataggcggc 1800
53 ctggataaaa tagacttgaa cgaactggaag tcgaacacgc ggctgaagca ctgtgtggcc 1860
54 gacagcaaca tcgtgcggtg gttctggcaa gcggtggaga cgttcgatga agaaaggagg 1920
55 gccaggctcc tgcagtttgt gaactgggtcc acgcgagtc cgtccaagg ctccaaggct 1980
56 ttgcaaggtt ctacaggcgc ggcaggggccc cggctgttca ccatccaact gatagacgcg 2040
57 aacacagaca accttcogaa ggccataacc tgctttaacc ggatcgacat tccacccatat 2100
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67 <223> OTHER INFORMATION: Human Smurf1
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73 Leu Ala Lys Lys Asp Phe Phe Arg Leu Pro Asp Pro Phe Ala Lys Ile
74 20 25 30
76 Val Val Asp Gly Ser Gly Gln Cys His Ser Thr Asp Thr Val Lys Asn
77 35 40 45
79 Thr Leu Asp Pro Lys Trp Asn Gln His Tyr Asp Leu Tyr Val Gly Lys
80 50 55 60
82 Thr Asp Ser Ile Thr Ile Ser Val Trp Asn His Lys Lys Ile His Lys
83 65 70 75 80
85 Lys Gln Gly Ala Gly Phe Leu Gly Cys Val Arg Leu Leu Ser Asn Ala
86 85 90 95
88 Ile Ser Arg Leu Lys Asp Thr Gly Tyr Gln Arg Leu Asp Leu Cys Lys
89 100 105 110
91 Leu Asn Pro Ser Asp Thr Asp Ala Val Arg Gly Gln Ile Val Val Ser
92 115 120 125
94 Leu Gln Thr Arg Asp Arg Ile Gly Thr Gly Gly Ser Val Val Asp Cys
95 130 135 140
97 Arg Gly Leu Leu Glu Asn Glu Gly Thr Val Tyr Glu Asp Ser Gly Pro
98 145 150 155 160
100 Gly Arg Pro Leu Ser Cys Phe Met Glu Glu Pro Ala Pro Tyr Thr Asp
101 165 170 175
103 Ser Thr Gly Ala Ala Ala Gly Gly Gly Asn Cys Arg Phe Val Glu Ser
104 180 185 190
106 Pro Ser Gln Asp Gln Arg Leu Gln Ala Gln Arg Leu Arg Asn Pro Asp
107 195 200 205
109 Val Arg Gly Ser Leu Gln Thr Pro Gln Asn Arg Pro His Gly His Gln
110 210 215 220
112 Ser Pro Glu Leu Pro Glu Gly Tyr Glu Gln Arg Thr Thr Val Gln Gly
113 225 230 235 240
115 Gln Val Tyr Phe Leu His Thr Gln Thr Gly Val Ser Thr Trp His Asp
116 245 250 255
118 Pro Arg Ile Pro Arg Asp Leu Asn Ser Val Asn Cys Asp Glu Leu Gly

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119		260		265		270
121	Pro	Leu	Pro	Pro	Gly	Trp
122		275		280		285
124	Tyr	Phe	Val	Asp	His	Asn
125		290		295		300
127	Leu	His	His	Ile	Met	Asn
128	305			310		315
130	Pro	Leu	Pro	Leu	Pro	Ser
131				325		330
133	Ala	Gln	Arg	Tyr	Glu	Arg
134				340		345
136	His	Glu	Leu	Ser	Leu	Gln
137				355		360
139	Val	Ser	Arg	Glu	Glu	Ile
140				370		375
142	Met	Arg	Pro	Lys	Asp	Leu
143	385			390		395
145	Glu	Glu	Gly	Leu	Asp	Tyr
146				405		410
148	Leu	Cys	His	Glu	Met	Leu
149				420		425
151	Thr	Asp	Asn	Ile	Tyr	Met
152				435		440
154	Pro	Asp	His	Leu	Ser	Tyr
155				450		455
157	Ala	Val	Phe	His	Gly	His
158	465			470		475
160	Tyr	Lys	Gln	Leu	Leu	Gly
161				485		490
163	Val	Asp	Pro	Glu	Leu	His
164				500		505
166	Ile	Thr	Pro	Val	Leu	Asp
167				515		520
169	Gly	Arg	Ile	Leu	Gln	His
170				530		535
172	Val	Thr	Glu	Glu	Asn	Lys
173	545			550		555
175	Arg	Phe	Met	Arg	Gly	Ile
176				565		570
178	Phe	Asn	Glu	Leu	Ile	Pro
179				580		585
181	Glu	Leu	Glu	Leu	Ile	Ile
182				595		600
184	Trp	Lys	Ser	Asn	Thr	Arg
185				610		615
187	Val	Arg	Trp	Phe	Trp	Gln
188	625			630		635
190	Ala	Arg	Leu	Leu	Gln	Phe
191				645		650

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193 Gly Phe Lys Ala Leu Gln Gly Ser Thr Gly Ala Ala Gly Pro Arg Leu
194      660      665      670
196 Phe Thr Ile His Leu Ile Asp Ala Asn Thr Asp Asn Leu Pro Lys Ala
197      675      680      685
199 His Thr Cys Phe Asn Arg Ile Asp Ile Pro Pro Tyr Glu Ser Tyr Glu
200      690      695      700
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203 705      710      715      720
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209 <211> LENGTH: 2247
210 <212> TYPE: DNA
211 <213> ORGANISM: Homo sapiens
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Human Smurf2
216 <400> SEQUENCE: 3
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218 gcaaaaaac tggtaaaaa gattttttc cgacttctg atccatttg taaggctgtg      120
219 gttgatggat ttgggcaatg gcattctaca gatactgtg agaatacgc tgcattcaca      180
220 tggatacagc attatgacct gtatatggga aagctctgatt cagttacagt cagtgatagg      240
221 aatcaccaaga agatccataa gaaacaagg tctggatttc tcggttggtg tcgtcttctt      300
222 tccaatgccca tcaaccgcct caaagacact ggttatcaga ggttggtatt atgcacaact      360
223 gggccaatg acaatgatac agttagagga cagatagtag taagtcttca gtccagagac      420
224 cgaataggca caggaggaca agttgtggac tgcagtcgtt tatttgataa cgatttacca      480
225 gcggctgggg aagaaaggag aaccgcctct ggaagaatcc agtatctaaa ccataataca      540
226 agaactacgc aatgggagcg cccaacacga cgggcatccg aatattctag ccttggcaga      600
227 cctcttagct gctttgttga tgagaacaac ccaattagtg gaacaaatgg gcaacaatgt      660
228 ggacagtctt cagatccacg gctggcagag agggagatca ggtcacaaac acatagaaat      720
229 tacatgagca gaacacattt acatactcct ccagacotac cagaaggcta tgaacagagg      780
230 acaacgcgaac aaggccaggt gtatttctta catcacaga ctggtgtgag cacatggcat      840
231 gatccaagag tggccaggga tcttagcaac atcaattgtg aagagcttgg tccattggct      900
232 cctgcatggg agatccgtga tacggcaaca ggcagagttt atttctgtga ccatatacaac      960
233 agaacaacac aatttacaga tctctggctg ttctgtaact tgcatttaagt tttaaatcgg      1020
234 cagaaccaat tgaagacca acagcaacag caagtggatc cgttatgtcc tgcattgaca      1080
235 gaatgcctga cagtcacca gtaacaagca gacctggctc agaaactaaa aattttgcgg      1140
236 caagaacttt cccaacaaca gcctcaggca ggtcattgcc gcatgtagg tccacgggaa      1200
237 gaggattttt aggaatcata tcgacaggtc atgaaaatga gacaaaaaga tctctggaag      1260
238 cgataatgta taaaattttg tggagaagaa ggccttgact atggaggcgt tgcacgggaa      1320
239 tgggtgtatc tcttgtcaac tgaatatgtt aatccatact atggcctctt ccagattcca      1380
240 agagatgata tttatacatt gcagatcaat cctgattctg cagttaatcc ggaacattta      1440
241 tctatcttcc actttgttgg acgaataatg ggaatggctg tgttctatgg acatttatatt      1500
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243 gacatggagt tagtagatcc ggaattctac aacagtttag tgtggatact tgagaatgat      1620
244 attacaggtg ttttgaccca tacccttctg gttgaacata atgcataatt tgaaattatt      1680
245 cagcatgaac ttaaacccaa tggcaaaagt atccctgtta atgaagaaaa taaaagaaga      1740
246 tatgtcaggc tctatgtgaa ctggagattt ttacagagca ttgaggctca attcttggct      1800
247 ctgcagaaag gatttaatga agtaattcca caacatctgc tgaagacatt tgcattgaga      1860
248 gagttagaga tccattattg tggacttgga aagatagatg ttaattgact gaaggttaac      1920
249 acccggttaa aacactgtac accagacagc aacattgtca aatggttctg gaaagctgtg      1980

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252 caccagattg atgcctgcac taacaacctg ccgaaagccc acattgtt caatcgaata 2160
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257 <211> LENGTH: 748
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Human Smurf1
264 <400> SEQUENCE: 4
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271 Pro Asp Pro Phe Ala Lys Val Val Val Asp Gly Ser Gly Gln Cys His
272 35 40 45
274 Ser Thr Asp Thr Val Lys Asn Thr Leu Asp Pro Lys Trp Asn Gln His
275 50 55 60
277 Tyr Asp Leu Tyr Ile Gly Lys Ser Asp Ser Val Thr Ile Ser Val Trp
278 65 70 75 80
280 Asn Asn His Lys Lys Ile His Lys Lys Gln Gly Ala Gly Phe Leu Gly Cys
281 85 90 95
283 Val Arg Leu Leu Ser Asn Ala Ile Asn Arg Leu Lys Asp Thr Gly Tyr
284 100 105 110
286 Gln Arg Leu Asp Leu Cys Lys Leu Gly Pro Asn Asp Asn Asp Thr Val
287 115 120 125
289 Arg Gly Gln Ile Val Val Ser Leu Gln Ser Arg Asp Arg Ile Gly Thr
290 130 135 140
292 Gly Gly Gln Val Val Asp Cys Ser Arg Leu Phe Asp Asn Asp Leu Pro
293 145 150 155 160
295 Asp Gly Trp Glu Glu Arg Arg Thr Ala Ser Gly Arg Ile Gln Tyr Leu
296 165 170 175
298 Asn His Ile Thr Arg Thr Thr Gln Trp Glu Arg Pro Thr Arg Pro Ala
299 180 185 190
301 Ser Glu Tyr Ser Ser Pro Gly Arg Pro Leu Ser Cys Phe Val Asp Glu
302 195 200 205
304 Asn Thr Pro Ile Ser Gly Thr Asn Gly Ala Thr Cys Gly Gln Ser Ser
305 210 215 220
307 Asp Pro Arg Leu Ala Glu Arg Arg Val Arg Ser Gln Arg His Arg Asn
308 225 230 235 240
310 Tyr Met Ser Arg Thr His Leu His Thr Pro Pro Asp Leu Pro Glu Gly
311 245 250 255
313 Tyr Glu Gln Arg Thr Thr Gln Gln Gly Gln Val Tyr Phe Leu His Thr
314 260 265 270
316 Gln Thr Gly Val Ser Thr Trp His Asp Pro Arg Val Pro Arg Asp Leu
317 275 280 285
319 Ser Asn Ile Asn Cys Glu Glu Leu Gly Pro Leu Pro Pro Gly Trp Glu

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/14/2002
PATENT APPLICATION: US/10/009,945 TIME: 11:43:31

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,9,10,11,12,13